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Docket No.: PF-0181-2 CON
Inventors: Hillman et al.
Title: NOVEL HUMAN MEMBRANE PROTEIN
Serial No.: 09/898,216

#4

54	108	GAG	162 CCC P	216 CGA R	270 GTG V	324 CCT P	378 CTT L
CT.) 	GCT A	$ ext{TTG}$	GAG	CCT	GTG V	GTC V
ڻ L))	TTT F	GGA G	GTG V	ATC I	AAC N	GGA G
45 AGG	66	CCT P	153 TCT S	207 GTG V	261 CTC L	315 ATC I	369 GAT D
ָרָיָּרָי עלילי)))	0 0	TCC	TGG W	ATC I	GTC V	ATC
J L L		TGG W	GCC	GCC	AAC	ATT I	CAA Q
36 TGG	90,	CAC H	144 CGC R	198 GAG E	252 TTG L	306 GAA E	360 CTG L
J.	!))	999 9	9 9	CAG Q	GGT	AAG K	ACT T
T) T	 	CGG R	TCC	CAG	CCT	CTC	GTA V
27 TCG	81	GCG A	135 CGC R	189 CCG P	243 GAG E	297 AGT S	351 AAT N
رځي)))	GCG A	CCG	GTG V	CTG L	CAG Q	GAC D
JEJ) •	CGC R	TGG W	TTC	ATC I	GTG V	CTC
18	72	GCG A	126 TTC F	180 CTG	234 CGG R	288 TAT Y	342 ACT T
CNA	; ;	CTG L	3 9	GTA V	CAC H	CGA R	GTG V
ין טאַט		ATG M	ACT T	GTG V	TTC F	ATC I	GCT
0 کی ا	63	GAA	117 TCT S	171 ACC T	225 CGA R	279 CGG R	333 TCG S
) 1	TGG	CTC	AAC N		GAC D	CAG Q
ر ت))	990		171 CGA AAC ACC R N T	ATG M	TTA GAC L D	GAG
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FIGURE 1A

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432	o Ac	486	CTC	د.	540	GAT	0	704	ATC	ы	548	GAG	[+]	702	TCG	Ωĵ	756	GCA A	
	P - 1		AAA (GTG (_	GAG 7			GTG (GAG			GAA (E	
	GAC D		CGC			ATT			TAT	⋋		CAG			CGA			TCC	
423	E E	477	CIC	ıı	531	AGC	Ø	ת ת	CGT	K	639	ATG	Σ	693	ACC	H	747	GCC	
	0 1 0 C C C		GAG	臼		GCC	A		CIN	ᄓ		CAG	Ø		999			CTG L	
E.			TCA	S		AAT			TGC	ပ		ATG	Σ		GAG	Ш		ATC I	
414 TAC		468	AGA		522	CTG	гı		CGC		630	TCT	ß	684	$_{ m TCT}$	ß	738	CAG Q	ł
ر د	S S		ATG		•	\mathbf{I}^{CC}	ß		ATC			GAG	ы		GAG			GCC	
	A A		ACC	H		GAG			GGT	ტ		AAA	×		CTA	п		CAG Q	
405			ACA			SSS		7,97	TGG		621	GTG	>			>		AAA K	
	\ \ \		CAA	ø		GAA			TGC			CGG			ACA			AAG K	
	P		GCT			990			GAC	Д		CCC			CCC			GGG	
396	D D	450	CTA	ᆸ	504	TTC		ת מ	GCT	Ø	612	CCA	Д	999	CGG	民	720	GAA E	
A C			CAG	ø		GTC	>		GCT	Ø		\mathtt{GTG}	\wedge		AAA	×		GCA	
- ان 4) H		ACC	 H		AAA	×	. –	CAA	O	-	CAT	_ H		990	好		GTG V	
387	R S	441	GTC		495	GAC	Ω	549	AAC	z	603	ATC		657	SSS		711	AAT N	
t) L	Y L		CCC			NTG	×			н		GAT			GAG	臼		ATC	
T C	X X		TAT	≯		TCT	ഗ		၁၁၅	Ą		AAG	ĸ		GCA	Ø		GCC	:

FIGURE 1B

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810 GCG A	864 CAA Q	918 GCG A	972 GGC G	1026 CTC ACC AAA L T K	1080 AGA GAT GTC R D V	1134 AGT TAG S *
CTG	ACA T	AGC	CCT	ACC	GAT	AGT
GTT V	$^{ m CTG}$	GTC V	AAC CCT N	CTC	AGA R	ATG M
801 GCA A	855 GCT A	909 TAT Y	963 TCC S	1017 TAT GGA GCC C Y G A L	1071 AGC AGC 3	1125 GTC AAG V K
AGT	GCA	CAG Q	CCC	GGA G	1 AGC S	1 GTC V
GCC	GCT	GAG	CTG	TAT Y	99 (1)	CGA R
792 GAG E	846 CTG L	900 GCC A	954 CTA L	.008 GTA V	.062 AGT S	.116 GAT D
GGA	ATC	ACT GTG	ATC	1008 ATG GGT GTA 1 M G V	1062 CTC TCC AGT C L S S C	CTT L
GCA A	CGA R	ACT	ACT I	ATG M	CTC	GAA E
783 GCA A	837 ATT I	891 CTG L	945 TCC AAC I	999 CAG GCC A Q A N	1053 GAC TCA (D S I	1107 1116 GAT GAG GAA CTT GAT CGA D E E L D R
CAG Q	GCT À	TCA S	TCC	CAG Q	1 GAC D	1 GAT D
AAT N	GAA E	GCT	GAC D	GCT A	CCA	NTT X
774 ATA I	828 GCT A	882 GCA A	936 AAG K	990 GTG V	1044 ACT T	.098 AGT S
CAG Q	AAA K	GCA	GCC	ATG M	999	1098 GCA AGT 1 A S
GAA	GCT	GAT	CTG	AGC - S	CCA.	GAT
765 GCT A	819 AAG K	873 GGA G	927 AAA K	981 ACC T	.035 GTG V	.089 ACA T
AAG K	GCC	AAT N	927 TCC AAA S K	GTC V	CCA P	1 GGT G
765 GAA AAG GCT E K A	AAG GCC K A	873 CAT AAT GGA (H N G	TTC	981 GAT GTC ACC D V T	1035 GCC CCA GTG A P V	1089 CAG GGT ACA (Q G T

FIGURE 1C

IGURE 1D

1143 1152 1161 1170 1179 1188 TGG AGC TGG GCG AGT CTG GGG ACA AGG AAG CAG ATT TTC CTG ATT

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LARAARGHWG PEAEGLSTGFWPRS GR 789094 NLKTCSLSTH SELQKKNEKHDGNP SK GI 31069 EYGMPEGSYDSVFTYAPPYNDLDKMGYMGPARQGMMLGNK GI 1353669 QGA	V P Q Q E A W V V E R M G R F H R I L E P G L N I L I 789094 C I K I I K E Y E R A I I F R L G R I L Q G G A K G P G L F F I L GI 31069 C M K V V Q D E Y E R A V I F R L G R L I G G G A K G P G I F F V L GI 1065452 A L K F I S T S E K L V V L R L G R A Q K T R G P G I T L V I GI 1353669 S V A L I P Q A E A A V I E R L G R Y S R T V S G Q L T L L V Z79701 A I V I V N Q Y E G G L I F R L G R V I G K L K P G I N I I I GI 1591514	KVDMRTISFDIPPQEILTKDSVTLOIDGVLYL789094 KVDMRTISFDIPPQEILTKDSVTISVDGVVYY GI 31069 KVDLRTVSFSVPPQEILTKDSVTTSVDGVVYY GI 1065452 KVTMSITAFNVPPLQIITTDRGLVELGATVFL GI 1353669 RVDLRERVVSFPPQPVITEDNLTLNIDTVVYF Z79701 KVDMRTRVTDIPPQEMITKDNAVVKVDAVVY GI 1591514	A S Y G V E D P E Y A V T O L A Q T T M R S E L G K L S X D K V F 789094 A V A N I T N A D S A T R L L A Q T T L R N V L G T K N L S Q I L GI 31069 S V A N V E N A H H S T R L L A Q T T L R N M L G T R S L S E I L GI 1065452 A V C G V Q D R N A S V R T L A N T M L Y R Y I S K R I C D V T GI 1353669 A V X E I S N Y I V G V E Q L T T T L R N V V G G M T L E Q T L Z79701 A I L E V E D Y E X A I I N L A Q T T L R A I I G S M E L D E V L GI 1591514
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FIGURE 2A

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FIGURE 2E

789094. GI 31069 GI 1065452 GI 1353669 Z79701	789094 GI 31069 GI 1065452 GI 1353669
OAS X DEELD RVK L L	
330 <u>S.L.S.S.G.S.S.R.DVOG</u> <u>T.D.A.S.X.DE.E.L.D</u> <u>R.V.K.</u> 789094 276 L. GI 31069 276 S.G. 1065452 364 VVFE - T.S.L.E.VFGKILTKEVSPVTVYMNGNLK <u>VK</u> GSIQDAM GI 1353669 333 HAADGDDA.E.VAGWFSTDTDPSIARAVA TAEAIARKPV Z79701	355 M.S 277 Q - G I I G A K'H S H L G 277 D - G I S 403 Q L K H L V E R M S D W L 370 E - G S L G T P P R L T Q

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Library	Lib Description	Abun	Pct Abun
PROSTUT03	Drostate tumon 67 v		
COLNNOT05	prostate tumor, 67 M, match to PROSNOT05	2	0.0703
	colon, 40 M, match to COLNCRT01	2	0.0577
TESTNOT03	testis, 37 M	1	0.0557
LIVRNOT02	liver, 32 F	1	
HUVENOB01		1	0.0515
LVENNOT03	HUVEC endothelial cell line, control	1	0.0418
	heart, left ventricle, 31 M	1	0.0336
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	
KERANOT01	keratinocytes, neonatal M	1	0.0288
CRBLNOT01		1	0.0227
	brain, cerebellum, 69 M	1	0.0194
LUNGNOT04	lung, 2 M	1	0.0182
PGANNOT01	paraganglia, 46 M	1	
BRSTTUT01		1	0.0159
	breast tumor, 55 F, match to BRSTNOT02	1	0.0150